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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of: Attorney Docket No.: 2873-US

     Peter Robert Baum and William Christian Fanslow III

Serial No.:   09/778,187   Group Art Unit: 1644

Filed: February 06, 2001   Examiner: Roark, J. H.

For: MOLECULES DESIGNATED LDCAM

DECLARATION UNDER 37 C.F.R. §1.131

RECEIVED

Commissioner of Patents
P. O. Box 1450
Alexandria VA, 22313-1450

MAY 3 0 2003

TECH CENTER 1600/2900

Sir:

We, the undersigned, hereby declare that:

1. We are the same Peter Robert Baum and William Christian Fanslow III named as co-inventors on the above-identified application. Prior to December 03, 1997, a nucleic acid encoding human LDCAM was isolated, the sequence of said nucleic acid was determined, and the amino acid sequence encoded by said nucleic acid was deduced, in the United States of America by us, the co-inventors named in the subject application, as evidenced by the Exhibit enclosed herewith.

2. The nucleic acid and amino acid sequence data presented in the Exhibit were obtained and the works that generated those data were completed in this country prior to December 03, 1997. The amino acid sequence presented in the Exhibit (HuB7L1-CoR) is identical to SEQ ID NO: 2 of the instant application, which is the amino acid sequence of human LDCAM.

3. We therefore submit that this showing of facts is sufficient in character and weight as to establish that the invention of this application was reduced to practice prior to December 03, 1997, the earliest possible 102(e) date of the cited publication, U.S. Patent Application Publication US 2002/0198147 A1.

4. We further declare that all statements made herein of our own knowledge are true, and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both,

under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

5.22.03

Date

Peter Robert Baum

5-23-03

Date

William Christian Fanslow III

EXHIBIT

HuB7L1-CoR Full Length

(Linear) (Six Base) MAP of: 4469-Wi26.Seq check: 1995 from: 1 to: 1535
[hollingsworth.cncdna.4469]
req 4469 HuB7L1 counterstructure Wi26 pool314-28#34 FINAL SEQUENCE FILE
3mGel1648, #7046, #5080 / 3mGel1663 dpc7266,67 /2mGel1671 dpc7305,6
4469-wi26

```
       B                                           B
       ENXs               B                        aX
       aomi               c                        mh
       etaE               g                        Ho
       1131               l                        12
       //          Sal-22778 →                     /
       GCGGCCGCGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGCGGCA
     1 ---------+---------+---------+---------+---------+---------+ 60
       CGCCGGCGCGGGCTGTACCGCTCACATCACGACGGCTCGCCTAGGGTCACACGCCGCCGT
a                    M  A  S  V  V  L  P  S  G  S  Q  C  A  A  A  -


                              B
                              s
       N          B     B     p
       s          BsKNH AsBSX Bl                         ES  D
       p          aaaaa vrgmm a2                         aa  s
       B          nHsre aFlaa n8                         rp  a
       2          11112 11111 26                         11  1
                    //   / //  /                           /
       GCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCC
    61 ---------+---------+---------+---------+---------+---------+ 120
       CGCCGCCGCCGCCGCGGAGGGCCCGAGGCCGAGGCCGAAGACGACAACGAGAAGAGGCGG
a      A  A  A  A  A  P  P  G  L  R  L  R  L  L  L  L  L  F  S  A  -


       N                          A
       sS                         l
       ps                         w
       Bt                         N
       22                         1
       GCGGCACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATC
   121 ---------+---------+---------+---------+---------+---------+ 180
       CGCCGTGACTAGGGGTGTCCACTACCCGTCTTAGACAAATGCTTTCTGCACTGTCACTAG
a       A  A  L  I  P  T  G  D  G  Q  N  L  F  T  K  D  V  T  V  I  -
       Signal seq.      ^
       GAGGGAGAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAG
   181 ---------+---------+---------+---------+---------+---------+ 240
       CTCCCTCTCCAACGCTGGTAGTCAACGGTTCAGTTATTCTCACTGCTGAGACACTAAGTC
a      E  G  E  V  A  T  I  S  C  Q  V  N  K  S  D  D  S  V  I  Q  -


                        E
       A                c                        B
       l                o              S         s
       w                5              t         p
       N                7              u         M
```

```
                 1                1                    1   1
      CTACTGAATCCCAACAGGCAGACCATTTATTTCAGGGACTTCAGGCCTTTGAAGGACAGC
  241 ---------+---------+---------+---------+---------+---------+ 300
      GATGACTTAGGGTTGTCCGTCTGGTAAATAAAGTCCCTGAAGTCCGGAAACTTCCTGTCG
    a     L  L  N  P  N  R  Q  T  I  Y  F  R  D  F  R  P  L  K  D  S   -


                 A
                 l     A                                    P      B
                 w     p                                    s      s
                 N     o                                    h      m
                 1     1                                    A      B
                                                            1      1
         #30518 (7A) →
      AGGTTTCAGTTGCTGAATTTTTCTAGCAGTGAACTCAAAGTATCATTGACAAACGTCTCA
  301 ---------+---------+---------+---------+---------+---------+ 360
      TCCAAAGTCAACGACTTAAAAAGATCGTCACTTGAGTTTCATAGTAACTGTTTGCAGAGT
    a     R  F  Q  L  L  N  F  S  S  S  E  L  K  V  S  L  T  N  V  S   -


         #30509 (1A/6A) →                                    #30516
      ATTTCTGATGAAGGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTAC
  361 ---------+---------+---------+---------+---------+---------+ 420
      TAAAGACTACTTCCTTCTATGAAAACGGTCGAGATATGGCTAGGGGGTGTCCTTTCAATG
    a     I  S  D  E  G  R  Y  F  C  Q  L  Y  T  D  P  P  Q  E  S  Y   -


                             B                    B   E
                 X           s                    C   s   c
                 c           a                    l   a   o
                 m           A                    a   a   B   R
      (5A) →     1           1                    1   1   5
      ACCACCATCACAGTCCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACT
  421 ---------+---------+---------+---------+---------+---------+ 480
      TGGTGGTAGTGTCAGGACCAGGGTGGTGCATTAGACTACTAGCTATAGGTCTTTCTGTGA
    a     T  T  I  T  V  L  V  P  P  R  N  L  M  I  D  I  Q  K  D  T   -


                             H
                 B           i                    E   B
                 s           n                    a   a
                 g           c                    e   l
                 1           2                    1   1
                        #30514 (4A) →
      GCGGTGGAAGGTGAGGAGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACG
  481 ---------+---------+---------+---------+---------+---------+ 540
      CGCCACCTTCCACTCCTCTAACTTCAGTTGACGTGACGATACCGGTCGTTCGGTCGGTGC
    a     A  V  E  G  E  E  I  E  V  N  C  T  A  M  A  S  K  P  A  T   -

                                                  E
                                                  a
                                                  r
                                                  1
      ACTATCAGGTGGTTCAAAGGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGG
  541 ---------+---------+---------+---------+---------+---------+ 600
      TGATAGTCCACCAAGTTTCCCTTGTGTCTCGATTTTCCGTTTAGCCTCCACCTTCTCACC
       ← #30517 (5B/6B/7B)
```

```
a       T   I   R   W   F   K   G   N   T   E   L   K   G   K   S   E   V   E   E   W   -
                                                            B
                                                            s
                    N                       N           A   pH              E
            A       s                       sP          p   1g              c
            f       p                       pv          a   2i              o   D   D
            l       H                       Bu          L   8A              5   r   r
            3       1                       22          1   61              7   d   a
                                                                            1   1   2
                    /                                       /
        TCAGACATGTACACTGTGACCAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGG
601     ---------+---------+---------+---------+---------+---------+ 660
        AGTCTGTACATGTGACACTGGTCAGTCGACTACGACTTCCACGTGTTCCTCCTGCTACCC
a       S   D   M   Y   T   V   T   S   Q   L   M   L   K   V   H   K   E   D   D   G   -
```

```
                            B
                            s
        P                   pH
        p   P               1g                  S   P       B   N
        u   s               2i                  f   s       s   s
        M   s               8A                  c   t       p   p
        1   1               61                  1   1       M   B
        /                   /                               1   2
        GTCCCAGTGATCTGCCAGGTGGAGCACCCTGCGGTCACTGGAAACCTGCAGACCCAGCGG
661     ---------+---------+---------+---------+---------+---------+ 720
        CAGGGTCACTAGACGGTCCACCTCGTGGGACGCCAGTGACCTTTGGACGTCTGGGTCGCC
a       V   P   V   I   C   Q   V   E   H   P   A   V   T   G   N   L   Q   T   Q   R   -
```

```
                            B
                            s
                    A       pH
        X           S       p   1g                          E
        b           m       a   2i                          c
        a           l       L   8A                          o
        1           1       1   61                          N
                                /                           1
        TATCTAGAAGTACAGTATAAGCCTCAAGTGCACATTCAGATGACTTATCCTCTACAAGGC
721     ---------+---------+---------+---------+---------+---------+ 780
        ATAGATCTTCATGTCATATTCGGAGTTCACGTGTAAGTCTACTGAATAGGAGATGTTCCG
                                ← #30515 (4B)
a       Y   L   E   V   Q   Y   K   P   Q   V   H   I   Q   M   T   Y   P   L   Q   G   -
```

```
            B
        AsSX                S           H   N
        vrmm                m           iHA s
        aFaa                l           npf p
        1111                1           cal H
        / /                             213 1
                                        /
        TTAACCCGGGAAGGGGACGCGCTTGAGTTAACATGTGAAGCCATCGGGAAGCCCCAGCCT
781     ---------+---------+---------+---------+---------+---------+ 840
        AATTGGGCCCTTCCCCTGCGCGAACTCAATTGTACACTTCGGTAGCCCTTCGGGGTCGGA
```

```
a        L  T  R  E  G  D  A  L  E  L  T  C  E  A  I  G  K  P  Q  P   -

         GTGATGGTAACTTGGGTGAGAGTCGATGATGAAATGCCTCAACACGCCGTACTGTCTGGG
    841  ---------+---------+---------+---------+---------+---------+ 900
         CACTACCATTGAACCCACTCTCAGCTACTACTTTACGGAGTTGTGCGGCATGACAGACCC
a        V  M  V  T  W  V  R  V  D  D  E  M  P  Q  H  A  V  L  S  G   -

         B
         s
         p                                              N     H
         AB1                                            s     i
         pa2                                            p     n
         an8                                            B     d
         126                                            2     3
         //
         CCCAACCTGTTCATCAATAACCTAAACAAAACAGATAATGGTACATACCGCTGTGAAGCT
    901  ---------+---------+---------+---------+---------+---------+ 960
         GGGTTGGACAAGTAGTTATTGGATTTGTTTTGTCTATTACCATGTATGGCGACACTTCGA-
         (-ggatatcactcagcataatgtata t7 Promoter)
a        P  N  L  F  I  N  N  L  N  K  T  D  N  G  T  Y  R  C  E  A   -

                                                41-mer  33713
```

```
                                                       B
                                                       s
                           T                           t
                           t                           A Z
                           h                           c 1
                           3                           c 7
         #30511 (2A/3A) →                              11
         TCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATACGATCCCCCCACA
    961  ---------+---------+---------+---------+---------+---------+ 1020
         AGTTTGTATCACCCCTTTCGAGTGAGCCTAATATACGACATACATATGCTAGGGGGGTGT
a        S  N  I  V  G  K  A  H  S  D  Y  M  L  Y  V  Y  D  P  P  T   -

         ACTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACCACCATCCTT
   1021  ---------+---------+---------+---------+---------+---------+ 1080
         TGATAGGGAGGAGGGTGTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTAGGAA
                                                  ← #30512 (2B)
a        T  I  P  P  P  T  T  T  T  T  T  T  T  T  T  T  T  T  I  L   -

              B
              s      A
              p      v
              M      a
              1      1
                                                    start T.M.
         ACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGATCATGCC
   1081  ---------+---------+---------+---------+---------+---------+ 1140
         TGGTAGTAGTGTCTAAGGGCTCGTCCACTTCTTCCGAGCTAGTCCCGTCACCTAGTACGG
         ←                   ← #30513 (3B)
```

a   T I I T D S R A G E E G S I R A V D H A -

```
                  B                       T
                  s                       t
                  a                       h
                  H                       3
                  1                       2
      GTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATTCTG
1141  ---------+---------+---------+---------+---------+---------+ 1200
      CACTAGCCACCGCAGCACCGCCACCACCACAAGCGGTACGACACGAACGAGTAGTAAGAC
a      V  I  G  G  V  V  A  V  V  V  F  A  M  L  C  L  L  I  I  L  -
```

```
            H                                     B
            a                                     s
            e                                     p
            2                                     H
                                                  1
      GGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT
1201  ---------+---------+---------+---------+---------+---------+ 1260
      CCCGCGATAAAACGGTCTGTATTTCCATGTATGAAGTGAGTACTTCGGTTTCCTCGGCTA
a      G  R  Y  F  A  R  H  K  G  T  Y  F  T  H  E  A  K  G  A  D  -
```

```
      GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACTCCGAA
1261  ---------+---------+---------+---------+---------+---------+ 1320
      CTGCGTCGTCTGCGTCTGTGTCGATATTAGTTACGTCTTCCTCCTGTCTTGTTGAGGCTT
                                              ← #30510 (1B)
a      D  A  A  D  A  D  T  A  I  I  N  A  E  G  G  Q  N  N  S  E  -
```

```
            S          X
            c          b
            a          a
            1          1
      GAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAATGAGGTGTCCAACTGGC
1321  ---------+---------+---------+---------+---------+---------+ 1380
      CTTTTCTTTCTCATGAAGTAGATCTAGTCGGAAAAACAAAGTTACTCCACAGGTTGACCG
a      E  K  K  E  Y  F  I  *
```

```
                                          A
                                          p
                                          o
                                          1
      CCTATTTAGATGATAAAGAGACAGTGATATTGGAACTTGCGAGAAATTCGTGTGTTTTTT
1381  ---------+---------+---------+---------+---------+---------+ 1440
      GGATAAATCTACTATTTCTCTGTCACTATAACCTTGAACGCTCTTTAAGCACACAAAAAA
```

```
      TATGAATGGGTGGAAAGGTGTGAGACTGGGAAGGCTTGGGATTTGCTGTGTAAAAAAAAA
1441  ---------+---------+---------+---------+---------+---------+ 1500
      ATACTTACCCACCTTTCCACACTCTGACCCTTCCGAACCCTAAACGACACATTTTTTTTT
```

```
                   B
                 ENXs
                 aomi
                 etaE
```

```
                                1131
                                 //
                AAAAAAATGTTCTTTGGAAAGAAAAAAGCGGCCGC
    1501    ---------+---------+---------+-----  1535
                TTTTTTTACAAGAAACCTTTCTTTTTTCGCCGGCG
```

Enzymes that do cut:

Acc1	Afl3	AlwN1	Apo1	Apa1	ApaL1	Ava1	Ba11
BamH1	Ban1	Ban2	Bcg1	Bgl1	BsaA1	BsaB1	BsaH1
Bsg1	BsiE1	BsmB1	Bsp1286	BspH1	BspM1	BsrF1	BstZ171
Cla1	Dra2	Drd1	Dsa1	Eae1	Ear1	Eco571	EcoN1
EcoR5	Hae2	HgiA1	Hinc2	Hind3	Hpa1	Kas1	Nar1
Not1	NspB2	NspH1	PpuM1	PshA1	Pss1	Pst1	Pvu2
Sap1	Sca1	Sfc1	Sma1	Sml1	Sst2	Stu1	Tth32
Xba1	Xcm1	Xho2	Xma1	Xma3			

Enzymes that do not cut:

Aat2	Acl1	Afl2	Age1	Asc1	Ase1	Asp718	Asu2
Avr2	Bbs1	BciV1	Bcl1	Bgl2	Bpu11021	Bpm1	Bsa1
BsiW1	Bsm1	BspE1	BssH2	BstE2	BstX1	Bsu361	Dra1
Dra3	Eam1105	Eco473	EcoR1	Fse1	Fsp1	Kpn1	Mlu1
Mun1	Nco1	Nde1	NgoM1	Nhe1	Nru1	Nsi1	Pac1
PflM1	Pme1	Pml1	Pvu1	Rsr2	Sal1	Sfi1	SgrA1
SnaB1	Spe1	Sph1	Srf1	Sse8387	Ssp1	Sst1	Sty1
Swa1	Tth31	Xho1	Xmn1				